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Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-9 (cancelled)

Claim 10 (currently amended) ~~[[The]]~~ A method of Claim 9 correlating gene expression with genotype comprising:

selecting a first plurality of individuals with a first genotype and a second plurality of individuals with a second genotype; wherein the genotypes are the states of a SNP;  
obtaining a first plurality of gene expression profiles from the first plurality of individuals;

obtaining a second plurality of gene expression profiles from the second plurality of individuals;

comparing the first and second gene expression profiles; wherein the step of comparing further comprises a step of evaluating the difference in gene expression between the first and second genotypes; and wherein the step of evaluating comprises calculating a normalized difference in gene expression between the first and second genotypes[[.]]: and

indicating at least one gene whose expression segregates with the genotypes as the genes affected by the genotypes.

11. (original) The method of Claim 10 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{(E_{wt}^{avg} - E_{elo}^{avg})^c}{\sigma_{wt}^a \sigma_{elo}^b}$$

wherein:  $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;

$E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;

$E_{elo}^{avg}$  = average gene expression for heterozygous/homozygous mutant for

the gene;

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$\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;  
 $\sigma_{e/o}$  = standard deviation of gene expression of heterozygous/homozygous mutant for the gene; and  
 $a, b, c$  = sensitivity parameters.

12. (original) The method of Claim 10 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{|(E_{wt}^{avg} - E_{e/o}^{avg})|^c}{\sigma_{wt}^a \sigma_{e/o}^b}$$

wherein:  $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;  
 $E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;  
 $E_{e/o}^{avg}$  = average gene expression for heterozygous/homozygous mutant for the gene;  
 $\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;  
 $\sigma_{e/o}$  = standard deviation of gene expression of heterozygous/homozygous mutant for the gene; and  
 $a, b, c$  = sensitivity parameters.

Claim 13-33 (Cancelled)

34 (currently amended) [[The]] A computer readable medium of Claim 26 comprising computer-executable instructions for performing the method for correlating gene expression with genotypes comprising:

inputting a first plurality of gene expression profiles from a plurality of individuals with a first genotype; wherein the genotypes are the states of a SNP; and

inputting a second plurality of gene expression profiles from a plurality of individuals with a second genotype;

comparing the first and second gene expression profiles; and wherein said comparing step further comprises the step of evaluating the difference in gene expression between the first and second genotypes; and wherein the step of evaluating comprises

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calculating a normalized difference in gene expression between the first and second genotypes[.]); and

indicating at least one gene whose expression segregates with the genotypes as the genes affected by the genotypes.

35 (original) The computer readable medium of Claim 34 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{(E_{wt}^{avg} - E_{e/o}^{avg})^c}{\sigma_{wt}^a \sigma_{e/o}^b}$$

wherein:  
 $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;  
 $E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;  
 $E_{e/o}^{avg}$  = average gene expression for heterozygous/homozygous mutant for the gene;  
 $\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;  
 $\sigma_{e/o}$  = standard deviation of gene expression of heterozygous/homozygous mutant for the gene; and  
 $a, b, c$  = sensitivity parameters.

36. (original) The computer readable medium of Claim 34 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{|(E_{wt}^{avg} - E_{e/o}^{avg})|^c}{\sigma_{wt}^a \sigma_{e/o}^b}$$

wherein:  
 $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;  
 $E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;  
 $E_{e/o}^{avg}$  = average gene expression for heterozygous/homozygous mutant for the gene;  
 $\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;  
 $\sigma_{e/o}$  = standard deviation of gene expression of heterozygous/homozygous mutant for the gene; and  
 $a, b, c$  = sensitivity parameters.

37-45 (cancelled)

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46. (currently amended) [[The]] A system of Claim 45 for associating a genotype with gene expression comprising:  
a processor; and  
a memory coupled with the least one processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:  
obtaining a first plurality of gene expression profiles from a plurality of individuals with a first genotype;  
obtaining a second plurality of gene expression profiles from a plurality of individuals with a second genotype; wherein the genotypes are the states of a SNP;  
comparing the first and second gene expression profiles; wherein said comparing step further comprises a step of evaluating the difference in gene expression between the first and second genotypes; and wherein the step of evaluating comprises calculating a normalized difference in gene expression between the first and second genotypes[.]; and  
indicating at least one gene whose expression segregates with the genotypes as the genes affected by the genotypes.

47 (original) The system of Claim 46 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{(E_{wt}^{avg} - E_{e/o}^{avg})^c}{\sigma_{wt}^a \sigma_{e/o}^b}$$

wherein:  $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;  
 $E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;  
 $E_{e/o}^{avg}$  = average gene expression for heterozygous/homozygous mutant for the gene;  
 $\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;  
 $\sigma_{e/o}$  = standard deviation of gene expression of heterozygous/homozygous mutant for the gene; and  
 $a, b, c$  = sensitivity parameters.

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48. (original) The system of Claim 46 wherein the step of comparing comprises a step of calculating a SNPmetric for each SNP and each gene according to:

$$^{gene} \Gamma_{SNP} = \frac{|(E_{wt}^{avg} - E_{elo}^{avg})|^c}{\sigma_{wt}^a \sigma_{elo}^b}$$

wherein:  $^{gene} \Gamma_{SNP}$  = SNPmetric for a given gene;

$E_{wt}^{avg}$  = average gene expression for wild type SNP for the gene;

$E_{elo}^{avg}$  = average gene expression for heterozygous/homozygous mutant for

the gene;

$\sigma_{wt}$  = standard deviation of gene expression of wild type SNP for the gene;

$\sigma_{elo}$  = standard deviation of gene expression of heterozygous/homozygous

mutant for the gene; and

$a, b, c$  = sensitivity parameters.